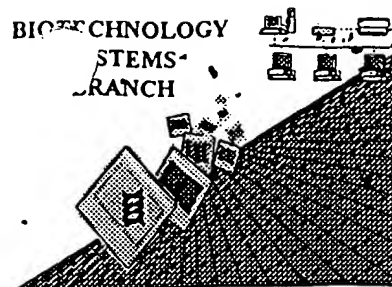# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/979,546_

Source: _PCT/09_

Date Processed by STIC: _12/4/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin3help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/779,546_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAF

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                                prevent "wrapping."

2_____Invalid Line Length,   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                                ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                                each n or Xaa can only represent a single residue. Please present the maximum number of each
                                residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                                previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                                the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                                Artificial or Unknown sequences.

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                                (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                                (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                                This sequence is intentionally skipped

                                Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
                                <400> sequence id number
                                000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                                In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                                is Artificial Sequence

11__√__Use of <220>   Sequence(s) _70_ missing   associated numeric identifiers and responses.
                                Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                                "Unknown." Please explain source of genetic material in <220> to <223> section.
                                (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                                listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                                any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

```
          RAW SEQUENCE LISTING                DATE: 12/04/2001
          PATENT APPLICATION:  US/09/979,546  TIME: 11:49:08

          Input Set : A:\Sequence.txt
          Output Set: N:\CRF3\11212001\I979546.raw
```

```
        3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W-->    4 <120> TITLE OF INVENTION: Novel Polypeptide
W-->    5 <130> FILE REFERENCE: 2609WOOP
C-->    6 <140> CURRENT APPLICATION NUMBER: US/09/979,546
        6 <141> CURRENT FILING DATE: 2001-11-20
        6 <150> PRIOR APPLICATION NUMBER: JP 11-140229
        7 <151> PRIOR FILING DATE: 1999-05-20
W-->    8 <160> NUMBER OF SEQ ID: 70
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
      956 <210> SEQ ID NO: 70
      957 <211> LENGTH: 44
      958 <212> TYPE: DNA
      959 <213> ORGANISM: Artificial Sequence
W-->  960 <220> FEATURE:
      961 <223> OTHER INFORMATION:              → see item 11 on Error Summary
W-->  962 <400> SEQUENCE: 70                                  Sheet
C-->  963 ctgggcgtcg acctgtgaca ggaagcccag gctcctgctc cact  44
E-->  965 1/35  delete
```

<223> needs
mandatory
response
whenever <213>
response is
Unknown or is
Artificial Sequence

FYI: all nucleotides
must be in
lower-case letters
when Sequence Listing
is in new Sequence Rules
format.

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/979,546**

DATE: 12/04/2001
TIME: 11:49:09

Input Set : **A:\Sequence.txt**
Output Set: **N:\CRF3\11212001\I979546.raw**

```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:127 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <400> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
L:232 M:283 W: Missing Blank Line separator, <400> field identifier
L:257 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:283 W: Missing Blank Line separator, <400> field identifier
L:301 M:283 W: Missing Blank Line separator, <400> field identifier
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:386 M:283 W: Missing Blank Line separator, <400> field identifier
L:401 M:283 W: Missing Blank Line separator, <400> field identifier
L:433 M:283 W: Missing Blank Line separator, <400> field identifier
L:434 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=16
L:445 M:283 W: Missing Blank Line separator, <400> field identifier
L:446 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=17
L:457 M:283 W: Missing Blank Line separator, <400> field identifier
L:458 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=18
L:474 M:283 W: Missing Blank Line separator, <400> field identifier
L:475 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=19
L:492 M:283 W: Missing Blank Line separator, <400> field identifier
L:493 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=20
L:506 M:283 W: Missing Blank Line separator, <400> field identifier
L:507 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=21
L:525 M:283 W: Missing Blank Line separator, <400> field identifier
L:526 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=22
L:543 M:283 W: Missing Blank Line separator, <400> field identifier
L:544 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=23
L:556 M:283 W: Missing Blank Line separator, <400> field identifier
L:557 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=24
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/979,546**

DATE: 12/04/2001
TIME: 11:49:09

Input Set : **A:\Sequence.txt**
Output Set: **N:\CRF3\11212001\I979546.raw**

```
L:568 M:283 W: Missing Blank Line separator, <400> field identifier
L:569 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=25
L:580 M:283 W: Missing Blank Line separator, <400> field identifier
L:581 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=26
L:594 M:283 W: Missing Blank Line separator, <400> field identifier
L:595 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=27
L:615 M:283 W: Missing Blank Line separator, <400> field identifier
L:616 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=28
L:624 M:283 W: Missing Blank Line separator, <400> field identifier
L:625 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=29
L:633 M:283 W: Missing Blank Line separator, <400> field identifier
L:634 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=30
L:648 M:283 W: Missing Blank Line separator, <220> field identifier
L:650 M:283 W: Missing Blank Line separator, <400> field identifier
L:651 M:112 C: (48) String data converted to lower case,
L:656 M:283 W: Missing Blank Line separator, <220> field identifier
L:658 M:283 W: Missing Blank Line separator, <400> field identifier
L:659 M:112 C: (48) String data converted to lower case,
L:664 M:283 W: Missing Blank Line separator, <220> field identifier
L:666 M:283 W: Missing Blank Line separator, <400> field identifier
L:667 M:112 C: (48) String data converted to lower case,
L:672 M:283 W: Missing Blank Line separator, <220> field identifier
L:674 M:283 W: Missing Blank Line separator, <400> field identifier
L:675 M:112 C: (48) String data converted to lower case,
L:680 M:283 W: Missing Blank Line separator, <220> field identifier
L:682 M:283 W: Missing Blank Line separator, <400> field identifier
L:683 M:112 C: (48) String data converted to lower case,
L:688 M:283 W: Missing Blank Line separator, <220> field identifier
L:690 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:112 C: (48) String data converted to lower case,
L:696 M:283 W: Missing Blank Line separator, <220> field identifier
L:698 M:283 W: Missing Blank Line separator, <400> field identifier
L:699 M:112 C: (48) String data converted to lower case,
L:704 M:283 W: Missing Blank Line separator, <220> field identifier
L:706 M:283 W: Missing Blank Line separator, <400> field identifier
L:707 M:112 C: (48) String data converted to lower case,
L:715 M:112 C: (48) String data converted to lower case,
L:723 M:112 C: (48) String data converted to lower case,
L:731 M:112 C: (48) String data converted to lower case,
L:739 M:112 C: (48) String data converted to lower case,
L:747 M:112 C: (48) String data converted to lower case,
L:755 M:112 C: (48) String data converted to lower case,
L:763 M:112 C: (48) String data converted to lower case,
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/979,546

DATE: 12/04/2001
TIME: 11:49:09

Input Set : **A:\Sequence.txt**
Output Set: **N:\CRF3\11212001\I979546.raw**

```
L:771 M:112 C: (48) String data converted to lower case,
L:779 M:112 C: (48) String data converted to lower case,
L:787 M:112 C: (48) String data converted to lower case,
L:795 M:112 C: (48) String data converted to lower case,
L:803 M:112 C: (48) String data converted to lower case,
L:965 M:254 E: No. of Bases conflict, LENGTH:Input:35 Counted:45 SEQ:70
L:965 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:965 M:252 E: No. of Seq. differs, <211>LENGTH:Input:44 Found:45 SEQ:70
```